WO 2004/029199

PCT/US2003/028654

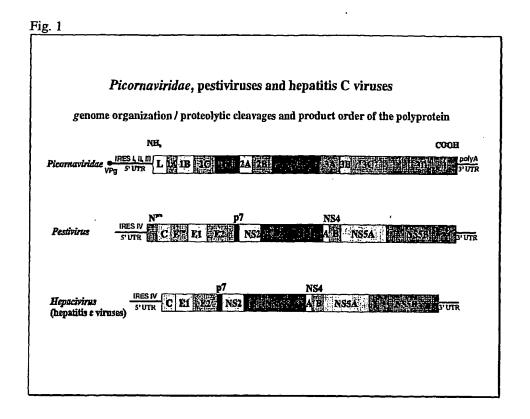
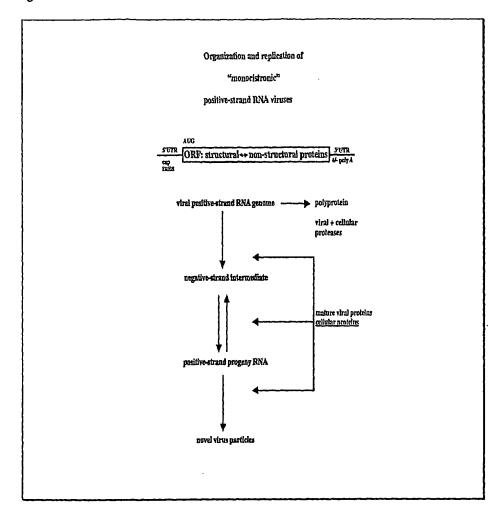


Fig.1B



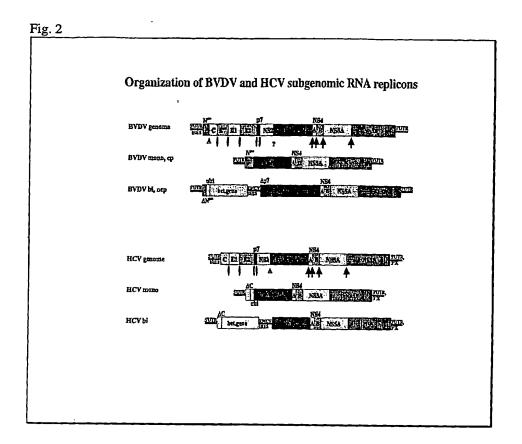
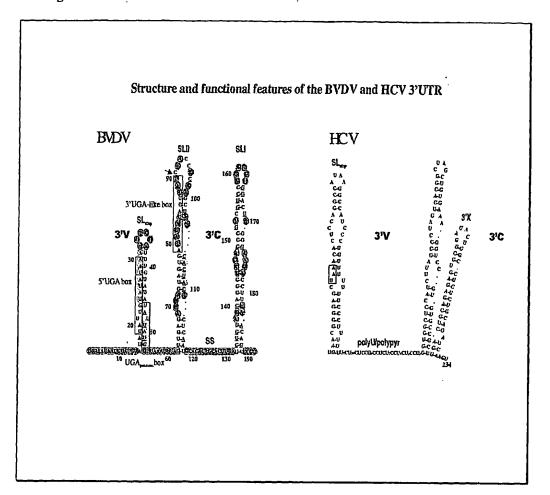
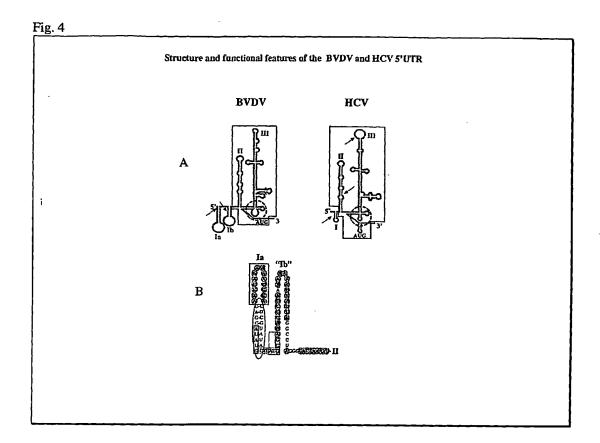
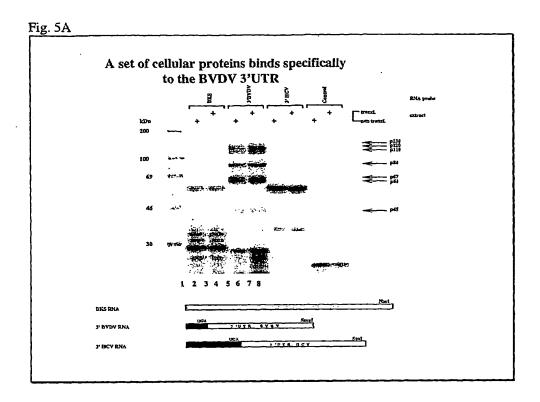


Fig. 3







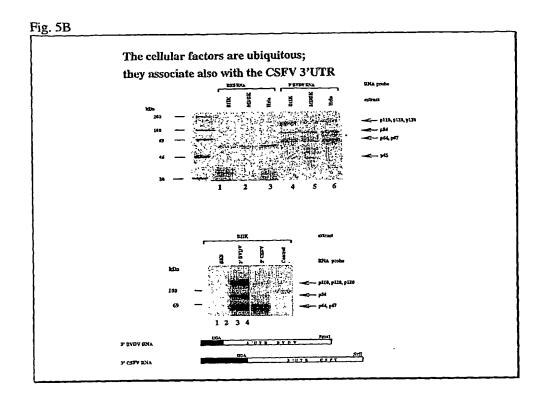


Fig. 5C

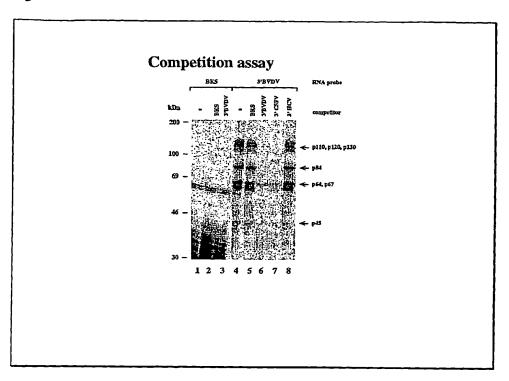


Fig. 5D Sequence alignment of pestiviral 3'V regions "UGA box" / position pestivirus strain BDV XSIS W AAU DOU AVA UAU SI BDV A841/3 46 GAU UOU AUAUAA 57 CSFV C-strain O UAU LOU AGAUAA 34 40 UAU UGU AAAUAA SA CSFV Alfort-T BVDV-1 NADL BVDV-1 Osloss O VAU VAU AVAŪAA 14 16 UAU UGU ACAUAA 27 M VAU VAU GUUVAA SI BVDV-1 CP7 IP U<u>N</u>U <u>U</u>GU AUA<u>UAA</u> 20 44 A&A UAU OGU O&A 57 BVDV-2 890 43 U<u>AU UGU</u> AUA<u>UAA</u>SA TE NVA TON VVV DVV 22 pseudo stop-codon" consensus sequence U A AUAU U U <u>аай</u> <u>и</u> а <u>A</u> A с с ссис G G 1 2 3 4 5 6 7 8 9 10 11 12

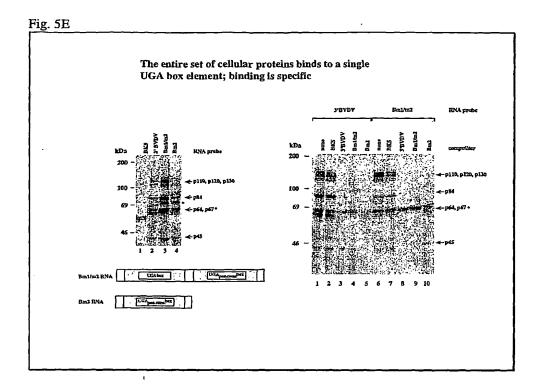
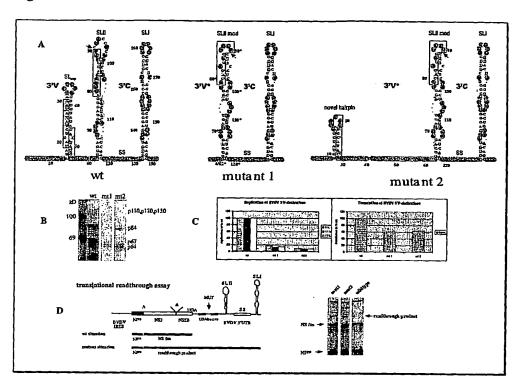
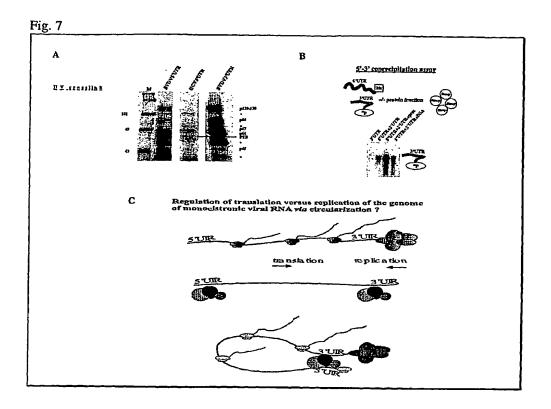


Fig. 6





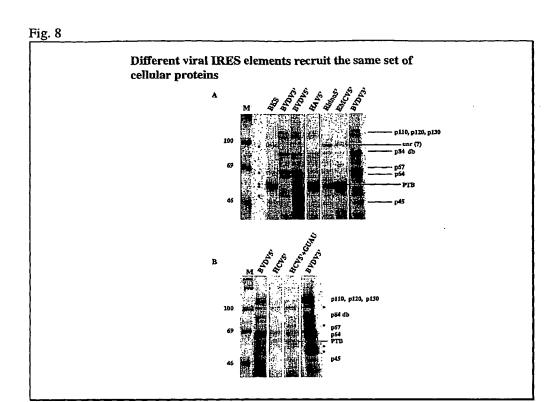
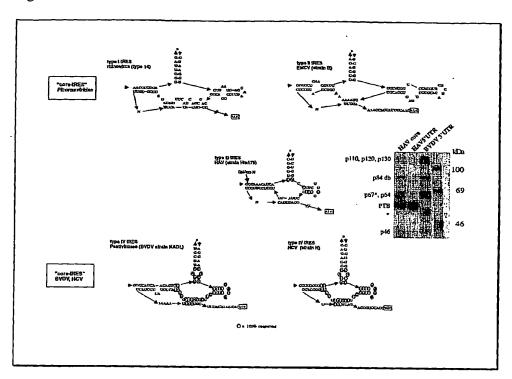


Fig. 9



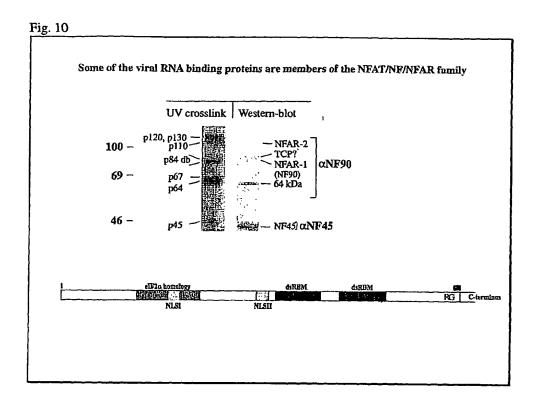
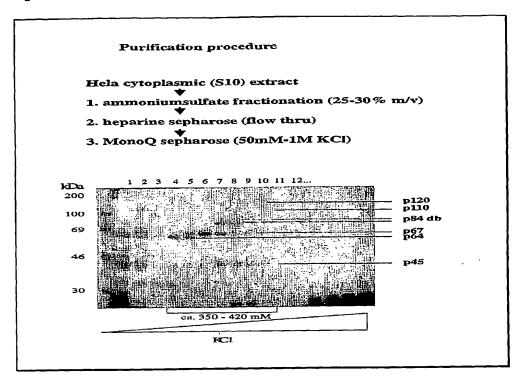


Fig. 10A



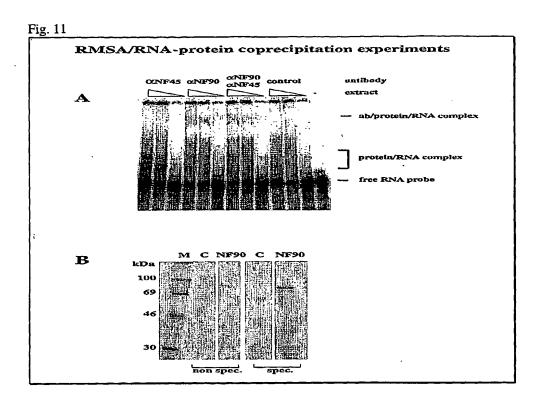
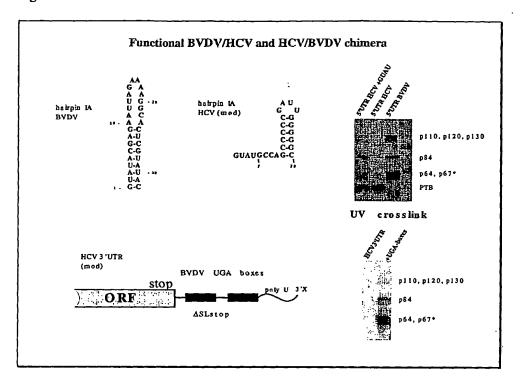
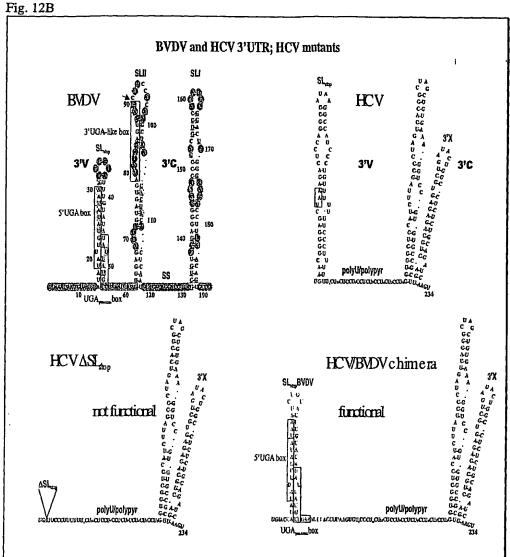


Fig. 12A



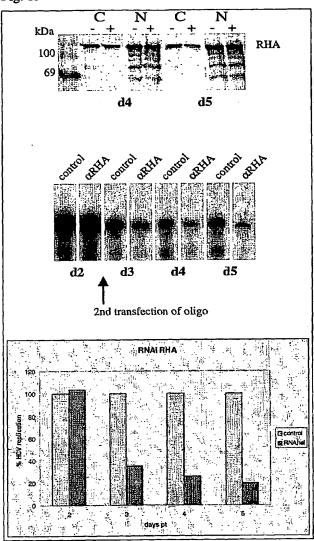




WO 2004/029199

PCT/US2003/028654

Fig. 13



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